

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 22:53:44 ; Search time 33.32 Seconds
(without alignments)
2110.117 Million cell updates/sec

Title: US-09-497-822a-19
Perfect score: 4912
Sequence: 1 MEYQLGLGRVYBRPPSKTYR..... SVQVPKILSGRKVPIYFHTQ 923

Scoring table: BL005M62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0⁸
Maximum Match 100⁸
Listing first 45 summaries
Database : PIR^{68,*}
1: Pir1:
2: Pir2:
3: Pir3:
4: Pir4:
5:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
1	4.880	99.3	919	A39248	androgen receptor
2	4.788	97.7	910	A34721	androgen receptor
3	4.763	97.0	911	B34721	androgen receptor
4	4.265	85.6	902	B40494	androgen receptor
5	4.176	85.0	899	A35895	androgen receptor
6	1.676	34.1	344	I51330	androgen receptor
7	1.523	31.0	848	JG0194	androgen receptor
8	1.262	25.7	930	A25923	progesterone receptor
9	1.262	25.7	933	QRH0P	progesterone receptor
10	1.234	25.1	923	I52080	progesterone receptor
11	1.218	24.8	786	A35466	progesterone receptor
12	1.205	24.5	923	A39396	progesterone receptor
13	1.092	22.2	981	A41401	mineralocorticoid receptor
14	1.078	22.0	984	A29513	glucocorticoid receptor
15	1.065	21.7	795	1 QRRNG	glucocorticoid receptor
16	1.063	21.7	783	A25651	glucocorticoid receptor
17	1.054	21.5	776	I54047	glucocorticoid receptor
18	1.042	21.2	777	1 QRHUGA	glucocorticoid receptor
19	1.023	20.8	758	S60386	glucocorticoid receptor
20	1.003	20.4	771	2 A54273	glucocorticoid receptor
21	9.43	19.2	742	.1 ORHUGB	glucocorticoid receptor
22	7.15	14.6	166	S35795	androgen receptor
23	5.02	10.2	595	2 I47140	estradiol receptor
24	4.91	10.0	586	1 ORXLE	estrogen receptor
25	4.85	9.9	600	1 QRRIUE	estrogen receptor
26	4.78	9.7	595	2 S60737	80K estrogen receptor
27	4.78	9.6	589	1 QRHE	estrogen receptor
28	4.74	9.6	599	1 QRHSE	estrogen receptor
29	4.74	9.6			estrogen receptor

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RESULT
B34721
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Accession
Govinda
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Title:
Referen
Accession
Molecule
Residue

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		RESULT	4		Db	277	PTCPAPLAECRKGSLLDDSAKSPTEDTAEYSPFKGGTYKGLGEFSLGCGSAAAGSSGTL	336
B40494		androgen receptor - rat			Qy	343	LPTSLSLXYSKSGALDEAAAYOSRDYNNPLLAGPPPPPPIPHARIKLENPDYGSWA	402
C;Species: Rattus norvegicus (Norway rat)		C;Date: 14-Feb-1992 #text_change 20-Sep-1999			Db	337	IPTSSLXYSKSGALDEAAAYOSRDYNNPLLAGPPPPPPIPHARIKLENPDYGSWA	396
C;Accession: B40494; A36283; B40108		R;Chang, C.; Kokontis, J.; Liao, S.			Qy	403	AAAACRYC6DASLHAGAGAGPGSGPSAASSSWHTLETAEFGOLYGPCCGGGGGG	462
R;Tan, J.; Joseph, D.R.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.		Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988			Db	397	AAAACRYC6DASLHGGSYAAPSISPPATASSWHTLETAEFGOLYGP-	445
Mol. Endocrinol. 2, 1276-1285, 1988		A;Title: Structural analysis of complementary DNA and amino acid sequences of human and mouse androgen receptor: primary structure, autorregulation of its messenger RNA			Qy	463	GGGGGGGGGGGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	522
A;Reference number: A40494; MUID:89017168		A;Accession: B40494			Db	446	--GGGGSSSSPSDAGQAPYGTTRPQLASQESDTPADWYPGGMVSRVPPYPSPTC	501
A;Status: preliminary		A;Molecule type: mRNA			Qy	523	VKSENGPWWMSGYGDMLRLEATDHVLPIDYFPPOKTCCLICGDEASGHYGA	582
A;Residues: 1-502 <CHA>		A;Cross-references: GB:M23264; PID:9202967; PID:AAA40759..1; PID:9202968			Db	502	VKSENGPWWMSGYGDMLRSDTRDHVLPIDYFPQPKTCLICGDEASGHYGA	561
R;Yarchoff, W.G.; Quaraby, V.E.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.		R;Chang, C.; Kokontis, J.; Liao, S.			Qy	583	CKVFVRAAKGOKYKLCAASNDCTIDKFRKNCPSCLRLRKCYEAGMTLJGARLKLGNLK	642
Mol. Endocrinol. 2, 1276-1285, 1988		A;Title: The rat androgen receptor: primary structure, autorregulation of its messenger RNA			Db	562	CKVFVRAAKGOKYKLCAASNDCTIDKFRKNCPSCLRLRKCYEAGMTLJGARLKLGNLK	621
A;Reference number: A34943; MUID:89112209		A;Accession: A34943			Qy	643	IQEEGFASSTTSPTTEETTQKLTUVTSHIEGCOPFLNVLATEIEFGVVA	702
A;Molecule type: mRNA		A;Cross-references: GB:A20133; PID:9202895; PID:AAA40733..1; PID:9202896			Db	622	GHDINQNQPDSEFA	681
A;Residues: 1-388; S', 390-902 <TAN>		R;Yarchoff, W.G.; Quaraby, V.E.; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; Sar, M.			Qy	703	AllSSSNELGRLQHVVKAKALPGERNHLVDOMAVTOYSWNGLMYFAMGWSFTNVN	762
A;Cross-references: GB:A20133; PID:9202895		J. Biol. Chem. 265, 8893-8900, 1990			Db	682	AllSSSNELGRLQHVVKAKALPGERNHLVDOMAVTOYSWNGLMYFAMGWSFTNVN	741
A;Title: A single base mutation in the androgen receptor gene causes androgen insensitivity syndrome		A;Title: A single base mutation in the androgen receptor gene causes androgen insensitivity syndrome			Qy	763	SRMLYFAPDLYNEYRMHKSMYSOCVRMHLSQEFGLCITPQEFLCMKALLFSLIPV	822
A;Reference number: A36283; MUID:90256822		A;Accession: A6283			Db	742	SRMLYFAPDLYNEYRMHKSMYSCVRMHLSQEFGLCITPQEFLCMKALLFSLIPV	801
A;Molecule type: mRNA		A;Cross-references: GB:J05454			Qy	823	DGLKNKOFFDELRMNYIKELDITACKKRKNPITSRRYFOLTKLDSVOTAREHQFTF	882
A;Residues: 1-194,196-902 <RAR>		R;Chang, C.; Kokontis, J.; Liao, S.			Db	802	DGLKNKOFFDELRMNYIKELDITACKKRKNPITSRRYFOLTKLDSVOTAREHQFTF	861
A;Cross-references: GB:J05454		Science 240, 324-326, 1988			Qy	883	DLLIKSHMVSVDFPEMMAITTSVQPKILSKGVKPYIFHFO	923
R;Chang, C.; Kokontis, J.; Liao, S.		A;Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor			Db	862	DLLIKSHMVSVDFPEMMAITTSVQPKILSKGVKPYIFHFO	902
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A;Residues: 540-611 <CH2>		R;Chang, C.; Kokontis, J.; Liao, S.						
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology		Science 240, 324-326, 1988						
C;Keywords: DNA binding; zinc finger		A;Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor						
F;540-598/domain: erba transforming protein homology <ERBA>		A;Reference number: A40108						
F;542-562/Region: zinc finger		A;Accession: B40108						
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	</td							

A; Accession: A37908 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-899 <HA> A; Cross-references: GB:S56585; NID:9236048; PIDN:AAB19916.1; PID:9236049 R; Faber, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Both, N.J.; Trapman, J. Biochem. J. 278, 269-278, 1991 A; Title: The mouse androgen receptor: Functional analysis of the protein and characterization A; Reference number: S17198; MUID:91354214 A; Accession: S34398 A; Molecule type: DNA A; Residues: 1-899 <FA2> A; Cross-references: EMBL:X59592; NID:949968; PIDN:CAA42160.1; PID:949969 R; He, W.W.; Kumar, M.V.; Tindall, D.J. Nucleic Acids Res. 19, 2373-2378, 1991 A; Title: A frame-shift mutation in the androgen receptor gene causes complete androgen insensitivity A; Reference number: S40626; MUID:91252278 A; Status: preliminary A; Molecule type: mRNA A; Residues: 366-413 <HEW> A; Cross-references: EMBL:X53779 R; Gaspar, M. Proc. Natl. Acad. Sci. U.S.A. 88, 8006-8010, 1991 A; Title: A single base deletion in the Tfm androgen receptor gene creates a short-lived allele A; Reference number: I49501; MUID:9220902 A; Accession: I49501 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-899 <RE5> A; Cross-references: GB:M37890; NID:9191935; PIDN:AAA37234.1; PID:9191936 C; Genetics: A; Introns: 518/2; 569/1; 608/1; 704/1; 752/2; 796/1; 848/3 C; Superfamily: unassigned erba-related proteins; erba transforming protein homology C; Key words: DNA binding; transcription regulation; zinc finger F; 536/Domain: regulatory #status predicted <REG> F; 539-559/Region: zinc finger F; 575-599/Region: zinc finger F; 650-899/Domain: hormone binding #status predicted <LIG>	Qy 345 STLSLYKSGALDEAAAYQSRDYYNEPIALAGPPPPPHARIKLEPLNDYGSAWAA 404 Db 336 SSLSLYKSGALDEAAAYQNRDYNFLPALSCLSPHPPPTPHARIKLEPLNDYGSAWAA 395 Qy 405 AACRYGDLASLHGAGAAAGPGSCGSPSAAASSSSHRPLFTAEGQLYGPCCGGGGGGGG 464 Db 396 AACRYGDLGSUHGSVAGSPNSGSPATSSSWHTLTFAEGLQYGP----- 442 Qy 465 GGGGGGGGGGEAGAVPYGTYRTPPQLAGQESDETTDPDWYDGGMYSRVPPYSPTCVK 524 Db 443 - -GGGESSSSPDAGPVAPYCYTRIPQGLTSOESYSASEWYEGGVINRVPSPNCVK 500 Qy 525 SEMGPWNDSYSSPYGMDMLERATDHLVPLIDYYPFPQKTLICGDDEASCHYGAUTCGSK 584 Db 501 SEMGPWNENSYSPYGDMLDSTRHVLPLIDYFPQKTLICGDDEASCHYGAUTCGSK 560 Qy 585 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 644 Db 561 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 620 Qy 645 EGEASSTSPTPEETTOKLTVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 704 Db 621 EEGENSAAGSPTEDPSQKMFVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 680 Qy 705 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 764 Db 681 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 740 Qy 765 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 824 Db 741 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 800 Qy 825 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 884 Db 801 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 860 Qy 885 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 923 Db 861 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 899 RESULT 6 I51330 androgen receptor - common canary (fragment)
Query Match 85.0% Score 4176; DB 2; Length 899; Best Local Similarity 84.1%; Pred. No. 2-1e-213; Matches 790; Conservative 40; Mismatches 53; Indels 56; Gaps 5;	C; Species: Serinus canaria (common canary) C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999 C; Accession: I51330 R; Nastiu, K.L.; Clayton, D.F. Endocrinology 134, 640-649, 1994 A; Title: Seasonal and tissue-specific regulation of canary androgen receptor messenger RNA A; Reference number: I51330; MUID:94130808 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-344 <NAS> A; Cross-references: GB:L25901; NID:9414733; PID:AAA17402.1; PID:9414734 A; Genes: AR C; Superfamily: unassigned erba-related proteins; erba transforming protein homology C; Keywords: zinc finger F; 1-251/Domain: erba transforming protein homology (fragment) <ERBA>
Query Match 34.1% Score 1676; DB 2; Length 344; Best Local Similarity 90.4%; Pred. No. 9.1e-82; Matches 311; Conservative 20; Mismatches 13; Indels 0; Gaps 0;	Qy 225 NYLGGTTSIDNAKELKAVSYMSGLGVEALEHLSPGEOLRGDCMYAPLJGPPAVRPT 284 Db 216 DSYLGGSNTDSAKELCKAVSYMSGLGVEALEHLSPGEQURGDCMYASLJGPPAVRPT 275 Qy 285 PCAPIAECRGSLLDSDSAGKSTTEAETSPFKGYTGTLEGESLGCGSSAAGASSCTLELP 344 Db 276 PCAPLPECKGLPDEGPKSTTEAETSSFKGYAKLEGESLGCGSSPAGSSCTLELP 335 Qy 345 STLSLYKSGALDEAAAYQSRDYYNEPIALAGPPPPPHARIKLEPLNDYGSAWAA 404 Db 336 SSLSLYKSGALDEAAAYQNRDYNFLPALSCLSPHPPPTPHARIKLEPLNDYGSAWAA 395 Qy 405 AACRYGDLASLHGAGAAAGPGSCGSPSAAASSSSHRPLFTAEGQLYGPCCGGGGGGGG 464 Db 396 AACRYGDLGSUHGSVAGSPNSGSPATSSSWHTLTFAEGLQYGP----- 442 Qy 465 GGGGGGGGGGEAGAVPYGTYRTPPQLAGQESDETTDPDWYDGGMYSRVPPYSPTCVK 524 Db 443 - -GGGESSSSPDAGPVAPYCYTRIPQGLTSOESYSASEWYEGGVINRVPSPNCVK 500 Qy 525 SEMGPWNDSYSSPYGMDMLERATDHLVPLIDYYPFPQKTLICGDDEASCHYGAUTCGSK 584 Db 501 SEMGPWNENSYSPYGDMLDSTRHVLPLIDYFPQKTLICGDDEASCHYGAUTCGSK 560 Qy 585 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 644 Db 561 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 620 Qy 645 EGEASSTSPTPEETTOKLTVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 704 Db 621 EEGENSAAGSPTEDPSQKMFVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 680 Qy 705 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 764 Db 681 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 740 Qy 765 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 824 Db 741 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 800 Qy 825 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 884 Db 801 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 860 Qy 885 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 923 Db 861 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 899 RESULT 6 I51330 androgen receptor - common canary (fragment)
Query Match 34.1% Score 1676; DB 2; Length 344; Best Local Similarity 90.4%; Pred. No. 9.1e-82; Matches 311; Conservative 20; Mismatches 13; Indels 0; Gaps 0;	Qy 225 NYLGGTTSIDNAKELKAVSYMSGLGVEALEHLSPGEOLRGDCMYAPLJGPPAVRPT 284 Db 216 DSYLGGSNTDSAKELCKAVSYMSGLGVEALEHLSPGEQURGDCMYASLJGPPAVRPT 275 Qy 285 PCAPIAECRGSLLDSDSAGKSTTEAETSPFKGYTGTLEGESLGCGSSAAGASSCTLELP 344 Db 276 PCAPLPECKGLPDEGPKSTTEAETSSFKGYAKLEGESLGCGSSPAGSSCTLELP 335 Qy 345 STLSLYKSGALDEAAAYQSRDYYNEPIALAGPPPPPHARIKLEPLNDYGSAWAA 404 Db 336 SSLSLYKSGALDEAAAYQNRDYNFLPALSCLSPHPPPTPHARIKLEPLNDYGSAWAA 395 Qy 405 AACRYGDLASLHGAGAAAGPGSCGSPSAAASSSSHRPLFTAEGQLYGPCCGGGGGGGG 464 Db 396 AACRYGDLGSUHGSVAGSPNSGSPATSSSWHTLTFAEGLQYGP----- 442 Qy 465 GGGGGGGGGGEAGAVPYGTYRTPPQLAGQESDETTDPDWYDGGMYSRVPPYSPTCVK 524 Db 443 - -GGGESSSSPDAGPVAPYCYTRIPQGLTSOESYSASEWYEGGVINRVPSPNCVK 500 Qy 525 SEMGPWNDSYSSPYGMDMLERATDHLVPLIDYYPFPQKTLICGDDEASCHYGAUTCGSK 584 Db 501 SEMGPWNENSYSPYGDMLDSTRHVLPLIDYFPQKTLICGDDEASCHYGAUTCGSK 560 Qy 585 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 644 Db 561 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 620 Qy 645 EGEASSTSPTPEETTOKLTVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 704 Db 621 EEGENSAAGSPTEDPSQKMFVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 680 Qy 705 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 764 Db 681 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 740 Qy 765 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 824 Db 741 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 800 Qy 825 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 884 Db 801 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 860 Qy 885 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 923 Db 861 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 899 RESULT 6 I51330 androgen receptor - common canary (fragment)
Query Match 34.1% Score 1676; DB 2; Length 344; Best Local Similarity 90.4%; Pred. No. 9.1e-82; Matches 311; Conservative 20; Mismatches 13; Indels 0; Gaps 0;	Qy 225 NYLGGTTSIDNAKELKAVSYMSGLGVEALEHLSPGEOLRGDCMYAPLJGPPAVRPT 284 Db 216 DSYLGGSNTDSAKELCKAVSYMSGLGVEALEHLSPGEQURGDCMYASLJGPPAVRPT 275 Qy 285 PCAPIAECRGSLLDSDSAGKSTTEAETSPFKGYTGTLEGESLGCGSSAAGASSCTLELP 344 Db 276 PCAPLPECKGLPDEGPKSTTEAETSSFKGYAKLEGESLGCGSSPAGSSCTLELP 335 Qy 345 STLSLYKSGALDEAAAYQSRDYYNEPIALAGPPPPPHARIKLEPLNDYGSAWAA 404 Db 336 SSLSLYKSGALDEAAAYQNRDYNFLPALSCLSPHPPPTPHARIKLEPLNDYGSAWAA 395 Qy 405 AACRYGDLASLHGAGAAAGPGSCGSPSAAASSSSHRPLFTAEGQLYGPCCGGGGGGGG 464 Db 396 AACRYGDLGSUHGSVAGSPNSGSPATSSSWHTLTFAEGLQYGP----- 442 Qy 465 GGGGGGGGGGEAGAVPYGTYRTPPQLAGQESDETTDPDWYDGGMYSRVPPYSPTCVK 524 Db 443 - -GGGESSSSPDAGPVAPYCYTRIPQGLTSOESYSASEWYEGGVINRVPSPNCVK 500 Qy 525 SEMGPWNDSYSSPYGMDMLERATDHLVPLIDYYPFPQKTLICGDDEASCHYGAUTCGSK 584 Db 501 SEMGPWNENSYSPYGDMLDSTRHVLPLIDYFPQKTLICGDDEASCHYGAUTCGSK 560 Qy 585 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 644 Db 561 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 620 Qy 645 EGEASSTSPTPEETTOKLTVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 704 Db 621 EEGENSAAGSPTEDPSQKMFVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 680 Qy 705 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 764 Db 681 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 740 Qy 765 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 824 Db 741 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 800 Qy 825 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 884 Db 801 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 860 Qy 885 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 923 Db 861 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 899 RESULT 6 I51330 androgen receptor - common canary (fragment)
Query Match 34.1% Score 1676; DB 2; Length 344; Best Local Similarity 90.4%; Pred. No. 9.1e-82; Matches 311; Conservative 20; Mismatches 13; Indels 0; Gaps 0;	Qy 225 NYLGGTTSIDNAKELKAVSYMSGLGVEALEHLSPGEOLRGDCMYAPLJGPPAVRPT 284 Db 216 DSYLGGSNTDSAKELCKAVSYMSGLGVEALEHLSPGEQURGDCMYASLJGPPAVRPT 275 Qy 285 PCAPIAECRGSLLDSDSAGKSTTEAETSPFKGYTGTLEGESLGCGSSAAGASSCTLELP 344 Db 276 PCAPLPECKGLPDEGPKSTTEAETSSFKGYAKLEGESLGCGSSPAGSSCTLELP 335 Qy 345 STLSLYKSGALDEAAAYQSRDYYNEPIALAGPPPPPHARIKLEPLNDYGSAWAA 404 Db 336 SSLSLYKSGALDEAAAYQNRDYNFLPALSCLSPHPPPTPHARIKLEPLNDYGSAWAA 395 Qy 405 AACRYGDLASLHGAGAAAGPGSCGSPSAAASSSSHRPLFTAEGQLYGPCCGGGGGGGG 464 Db 396 AACRYGDLGSUHGSVAGSPNSGSPATSSSWHTLTFAEGLQYGP----- 442 Qy 465 GGGGGGGGGGEAGAVPYGTYRTPPQLAGQESDETTDPDWYDGGMYSRVPPYSPTCVK 524 Db 443 - -GGGESSSSPDAGPVAPYCYTRIPQGLTSOESYSASEWYEGGVINRVPSPNCVK 500 Qy 525 SEMGPWNDSYSSPYGMDMLERATDHLVPLIDYYPFPQKTLICGDDEASCHYGAUTCGSK 584 Db 501 SEMGPWNENSYSPYGDMLDSTRHVLPLIDYFPQKTLICGDDEASCHYGAUTCGSK 560 Qy 585 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 644 Db 561 VEFKRAEGKOKYLCASRNNDCTIDFRKNCPSCRLRKCYEAGMTLARKLKLGNLKQ 620 Qy 645 EGEASSTSPTPEETTOKLTVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 704 Db 621 EEGENSAAGSPTEDPSQKMFVSHLEGYECQIFLNVEIEPGVVCAGHDNNOPDSPAAL 680 Qy 705 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 764 Db 681 LSSLNLNEGEROLVHVVKWAKALPGERPNLHVDDOMAVIQSWMGLMVFAMGWSFTNVNSR 740 Qy 765 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 824 Db 741 MLYFADLVNEYRMHKSMYSCQVRMHLSQEFGWLOTTPOEFLCMKALLFSTIPIVDG 800 Qy 825 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 884 Db 801 LKNQKFDEELRMNTIKELDRITACKRKNPNTCSRRRFYOLTKLSDSYOPIARELHQFTEDL 860 Qy 885 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 923 Db 861 LIKSHMVSDDFPEMAEITSVQVKPKLISKVKVITYFTQ 899 RESULT 6 I51330 androgen receptor - common canary (fragment)

Db	180	AAHKVLPRLSPSRQLLPPSSGSPHPW-----AVKPSQQPAAV 218	A; Residues: 1-933 <KAS> A; Cross-references: EMBL:X511730 R; Kastner, P. Submitted to the EMBL Data Library, February 1990
QY	154	PDEDDSAAPSTISLLGTPFPLSSCSDAKLIDLSEASTMOLQOOQQCAVESEGSSESSGRA 213	A; Reference number: S12464 A; Accession: S12464 A; Molecule type: mRNA A; Residues: 1-343, 'T', 345-933 <KA2>
Db	219	QVDDEDSSE-----SEGTVGPILKGOPRALGGTAAGGAA 253	A; Cross-references: EMBL:X51130; PIDN:CAA36018..1; PID:935652 R; Misrahi, M.; Atger, M.; D'Auriol, L.; Loofelt, H.; Meriel, C.; Fridlansky, F.; Gui Biochem. Biophys. Res. Commun. 143, 740-748, 1987
QY	214	REAGAPISSKDNLYLGTTSTI-SDNAKELKRAVSVMGLVEALEHLSPGQQLRG ---D 268	A; Title: Complete amino acid sequence of the human progesterone receptor deduced from A; Reference number: A03245; MUID:87184565 A; Accession: A03245 A; Molecule type: mRNA A; Residues: 1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <MTS> A; Cross-references: GB:MI5176; PIDN:9189934; PIDN:AAA60081..1; PID:9189935
Db	254	PVASGAA-----GVALVKRSEFSAPVSLA-----EQDAVAPGSPSPLATSVVD 301	A; Gene: GBR A; Cross-references: GDB:119493; OMIM:264080 A; Molecule type: mRNA A; Residues: 1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <MTS> A; Cross-references: GB:MI5176; PIDN:9189934; PIDN:AAA60081..1; PID:9189935
QY	269	CWYAPLUGVPAPVTPCAPLECKGSLLDSSAGKST-----EDTAEYSPFKGG---- 317	C; Superfamily: progesterone receptor; erba transforming protein homology C; Keywords: alternative splicing; DNA binding; nucleus; phosphoprotein; steroid hormo
Db	302	FHVPILPILNHAFLATRTROLLE--GESYDGAAASPFVDFQRGSSASSSTPVAGGDFPD 359	F; 165-933/Product: progesterone receptor form B #status predicted <MA2> F; 165-933/Region: zinc finger, CCCC motif F; 60-622/Region: zinc finger, CCCC motif F; 681-933/Domain: steroid binding #status predicted <STB> F; 41/Binding site: phosphate (Int) (covalent) #status predicted F; 227, 234, 552, 793/Binding site: phosphate (Ser) (covalent) #status predicted F; 329, 371, 601/Binding site: phosphate (Tyr) (covalent) #status predicted
QY	318	-YTKGLGEGLGCSSGAAAGSSGTFLPSLTLKSYLSKGALDEAAQYSDROY----N 368	Query Match Score 25.7%; Best Local Similarity 34.3%; Pred. No. 2,1e-59; Matches 347; Conservative 123; Mismatches 326; Indels 216; Gaps 33;
Db	360	CTTYPDAEPK-----DDAFLPLYGDFO-PPAIIKKEEEAAARSPPRYLVAGANPAA 412	QY 38 GPRHEAAASAAP-----PGAA-----SLLLQQQQQQQQ 66 Db 8 GPRAPHYAGGPPSPEVSPILLGRPAAGFPFGQSOTSDTLPEVSAIPLSGLLFLPPRCQCG 67 QY 67 QQQQQQQQQQQQQQETSQQQQQEDGSPQAHRRGPGYL-VLDBEEQQPSQPSQA 124 Db 68 DPSDEKTQDOOSHSIDVEGAYSAEATRGAQGSSSSSSPEKDSLVLAPSPGQS 127 QY 125 LECHPERQCVPEGAAVAASKS--LPQQLPAPPDEDSSAAPSITSLSGPTFP-----GL 176 Db 128 -----QPSPACEVTSSWCLGPFLP-----EDPPAPAPATQRYLSPMSRSCKVGD 174 QY 177 SSCSADLKDLSE--ASTMOLL-----QQQQEAVS-EGSSSGAREAS 218 Db 175 SSGTAHHKVLPRLGSPARQLLPPASESPIWGAPVKPSQAAAEEVEEDSSESEESAG 234 QY 219 APTSSKDNYLGSTSTISDNAKELCKAVSVMGLG-----VEALEHLSPG 262 Db 235 PLIKGKPERALGAA--AGGAAACPGAAAGGVALKPKEDRSRESAPRVAEQDAPMA 292
QY	591	AGBKQKYLCAQRNDCTIDPRKRKNCPSCRLLRKCYEAGMTLGARKLKGLNLKLOEGEAS 650	QY 263 EQLRG---DCMYAPLLGVPDPAVRPTCPAPIAECGSSLDDSGRSSTDAYESPFEKGGY 318 Db 293 RSPLATTVMDFLHVPTL-----PLNHALLAARTQLLEDSE-----YDGAGAA 336 QY 709 NELGEROLVHYWKWAKALPGFRNLHVDDOMAVIQYSWMGLMVAMGWRSTFTNNNSRMILYF 768
Db	596	MEQHNQYLCAQRNDCLVDKRKNCPACLRKCKFKKENVRMRA LD AV 655	Db 319 TKLEGESLGSGS--AAAGSSGTLELP-----STLSY-----KSGALD 356 QY 716 NOLGEROLLSSVWKWSKSLPGRNLHDDQTLTQYSWMSLUMVFLGWSYKHSQMLYF 775
QY	651	STTSPT--EFTQKLUTVSHLEGYEQPIFNLVLEIAEPGVCAHDNNNODPSFAALISSL 708	Db 337 SAFAPRSPCCASSPPVAVGDFPDCAYPPDAEPKDDFQPPALKIKEBEEGA-- 394
Db	656	ALPQPQGIPNQESQRTIFSPSEQIQLPPLNLMSIEPTDVYASHDNTPKDTISSLLTSL 715	QY 357 EAAAYOSDRDYY-----NFPLLAGPPPPPWHARIKLENPLDYGSAWA AAAA 406 Db 395 EASAPRSPSYLIVAGNPAAFPDFPLP-----GPPCPPLP-----RAT 430
QY	709	NELGEROLVHYWKWAKALPGFRNLHVDDOMAVIQYSWMGLMVAMGWRSTFTNNNSRMILYF 768	A; Title: Two distinct estrogen-regulated promoters generate transcripts encoding the two
Db	716	NOLGEROLLSSVWKWSKSLPGRNLHDDQTLTQYSWMSLUMVFLGWSYKHSQMLYF 775	A; Reference number: S09971; MUID:90228361
QY	769	APDLVNEYRMHKSRYM SQCYMRHLSOEGWLQTPOBEFLCMKALLFSITIPVDGLKRNQ 828	A; Reference number: S09971; MUID:1603-1614, 1990
Db	776	APDLTLINEQRMKESSYSLCLTMQIPQEVFLKQVLSQEFKLCKVLLNLTLEGRLSQ 835	A; Molecule type: mRNA
QY	829	KFDEDELMNTKELDRILACKRKNPSTSRRKQKPTSQPIARELHOFTFDLIKS 888	RESULT 9
Db	836	SQEFMRSSVIRELKAIGURQGVYSSSORFYLTQKLLNHDLVKQTHLYCQLNTFTQS 895	QHUP Progesterone receptor form B - human
QY	889	HMSVDFPEMMAEIISVQVPKILSKVKDIFYH 921	N; Contains: progesterone receptor form A
Db	896	RALSVEFPEMSEVIAAQLPKILAGMVPKLFIH 928	C; Species: Homo sapiens (man)
		C; Date: 30-Jun-1987 #sequence revision 18-Nov-1994 #text_change 22-Jun-1999	
		C; Accession: S09971; S12464; A03245	
		R; Kastner, P.; Krust, A.; Turcotte, B.; Stropp, U.; Tora, L.; Gronemeyer, H.; Champon, E	
		F; EBO J. 9, 1603-1614, 1990	
		A; Title: Two distinct estrogen-regulated promoters generate transcripts encoding the two	
		A; Reference number: S09971; MUID:90228361	
		A; Molecule type: mRNA	

QY 904 SVQYPKILSGKVVKPLYFH 921
 Db 904 AAOQPKTLAGMVKLLEH 921

RESULT 11

A35466

Progesterone receptor form B - chicken

N;Contains: progesterone receptor form A

C;Species: Gallus gallus (chicken)

C;Cross-references: text_change 20-Aug-1999

C;Accession: A35466; SD06284; A40903; A24312; A40911; A61552

R;Jeltsch, J.M.; Turcotte, B.; Garnier, J.M.; Lerouge, T.; Gronemeyer, H.

J. Biol. Chem. 265, 3967-3974, 1990

A;Title: Characterization of multiple mRNAs originating from the chicken progesterone receptor gene

A;Accession: A35466; MUID:90154085

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-786 <JEL>

A;Cross-references: GB:M32732; GB:J05240; PIDN:AAA49011_1; PID:9212553

R;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.E.; Krozowski, J.M.; Tsai, M.Y.; Meyer, M.E.; Krozowski, J.M.; Tsai, M.J.; Beattie, W.G.; Toft, D.O.; Huckaby, C.S.;

Mol. Endocrinol. 1, 517-525, 1987

A;Title: The chicken progesterone receptor: sequence, expression and functional analysis

A;Reference number: SD06284; MUID:88166640

A;Molecule type: DNA

A;Residues: 1-786 <GRD>

A;Cross-references: EMBL:Y00092; PIDN:CAA66282_1; PID:963745

R;Conneely, O.M.; Dobson, A.D.W.; Tsai, M.J.; Beattie, W.G.; Toft, D.O.; Huckaby, C.S.;

Mol. Endocrinol. 1, 517-525, 1987

A;Title: Sequence and expression of a functional chicken progesterone receptor.

A;Reference number: A40903; MUID:91042592

A;Accession: A40903

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-64, 'E', 65-786 <CON>

A;Cross-references: GB:M37518

R;Conneely, O.M.; Sullivan, W.P.; Toft, D.O.; Birnbaum, M.; Cook, R.G.; Maxwell, B.L.;

J. Clin. Endocrinol. 105, 767-770, 1986

A;Title: Molecular cloning of the chicken progesterone receptor.

A;Accession: A24661; MUID:86289413

A;Molecule type: mRNA

A;Residues: 128-133, 'E', 135-147, 'E', 149-164 <CO2>

A;Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21

R;Jeltsch, J.M.; Krozowski, Z.; Quirin-Stricker, C.; Gronemeyer, H.; Simpson, R.J.; Garnier, J.M.; Hinrichs-Rosello, M.V.; Cook, R.G.; Schrader, W.T.; O'Malley, B.W.

Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986

A;Title: Cloning of the chicken progesterone receptor.

A;Reference number: A24312; MUID:862287271

A;Accession: A24312

A;Molecule type: mRNA

A;Residues: 417-490 <JE2>

A;Cross-references: GB:MI4280; PIDN:AAA49039_1; PID:9212608

R;Birnbaum, M.; Hinrichs-Rosello, M.V.; Cook, R.G.; Schrader, W.T.; O'Malley, B.W.

Mol. Endocrinol. 1, 249-259, 1987

A;Title: Chemical and antigenic properties of pure 108,000 molecular weight chick proges-

A;Reference number: A40911; MUID:88288199

A;Status: Preliminary

A;Molecule type: protein

A;Residues: 128-133, 'E', 135-147, 'E', 149-164-546-558 <BI>

R;Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.

Mol. Cell. Endocrinol. 52, 177-184, 1987

A;Title: Peptide sequencing of the chick oviduct progesterone receptor form B.

A;Accession: A61552

A;Molecule type: protein

A;Residues: 136-153, 168-174, 195-228, 526-537, 'X', 539, 546-563 <SM>

C;Genetics: 400/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3

C;Superfamily: progesterone receptor; erba transforming protein homology

C;Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
 F;1-766/Product: progesterone receptor form B #status predicted <MA>
 F;128-762/Product: progesterone receptor form A #status predicted <MA>
 F;419-682/Domain: erba transforming protein homology <ERBA>
 F;421-441/Region: zinc finger
 F;457-481/Region: zinc finger

Query Match 24 / 8%; Score 1218; DB 2; Length 786;
 Best Local Similarity 33.4%; Pred. No. 3..57; Mismatches 259; Indels 260; Gaps 30;
 Matches 325; Conservative 128; EE matches 59; EE status 260;

QY 13 RPPSKTYRGAFQNLFQSREVIONPGPR-HPEAAASAAPPAGASLLLQQQQQQQQQQQQQQ 71
 Db 10 RAPSSARDGV-----LLQAPPSSREAEQIDVALDG---LLYPSNSDEEEEEEENE 57

QY 72 QQQQQQQQQQETS PROQQQQQGEDGSPQAHRRGPTGVLLDDEQPSQPSALECHPER 131
 Db 58 EEEEEEEDRDQPSYR-----EEEEEEDRDQPSYR----- 85

QY 132 GCVEPGAAVAAASKGLPQDQUPADEDDAASP-----LSLGGTPEQLSSCSADLKDL 187
 Db 86 -----PGGSSLISKICLDSWL-----DTFLAPAAHAAPWLSLGPPEPV----- 121

QY 188 SEASTMOLLIQQQQQEAQSEG-SSSGRAEASGAPTSKDNYLGGTSTISDNAKELCKAVS 246
 Db 122 -EVVAPMGRGPEKAVIDGPAGPAGPSQPRGP-----LWPGDSLNVAVK 167

QY 247 VSMGLGEVERLEHLSLSPGEQIRGDCMYAPLGVPPAVRPIPCAPLAECKGSLLDSDAGKSTE 306
 Db 168 ARPG-PEDSENAP-----LPGAAERGEFPERDA----- 196

QY 307 DTAYFSPKGGITKGRLBESIGLGSQGAAQSSSTLEPLSTSLYKSALDEAAYOSRDY 366
 Db 197 -----GPGEGL-----APAAASPAAVE-----FGA-----GQDY 222

QY 367 YNFPLALAGAPPDPHPPPHARIKLENPLDYGSAWAAAACOGRYGDIALSHGAGAAGPGS 426
 Db 223 LHPPI-----LPLNSAFLASRTR QLLOVEATYDGSAGPFRS 258

QY 427 GSPSAAASSSWHITLEAAEGOLYGPCCGGGGGGG-----GGGGGGGGGGGG 475
 Db 259 -SPSVPAAD-----LAEYG-YPPPDQKGPEFAYGFQASFALKIKEEGVGLPAAAPPFLG 309

QY 476 GEAGAVAPYGYTRRPQQLAGQFSDFTA-----PDWVPPGAVSRVYPPS----- 519
 Db 310 AKA-----APADFAOPPR-AQOPSPSLECVLYKAEPPLPGAGPAAPADSLPSTSAPPGL 364

QY 520 -----PTCVKSEMGPWNMDSGSPY-GDMRILETARDIVLPIDYYFPQKTC 563
 Db 365 YSPFLGLNGHQALGEFPAVNLKEGLPL-----CPIPGLYVRPDTETSSQSFESTDFQKTC 421

QY 564 LJCGDEASGHCHYGAUTLCGSKVFKVRAEGKQYLCASNRDCTIDKFRNCPSCLRKCG 623
 Db 422 LJCGDEASGHCHYGVLTGCSKVFKVRAEMGHNYLAGRDCIVKIRNCPCRLRKCG 481

QY 624 YEGAMTLGARKLKLGNLK-----LOEGEASSSTSPTEETQKLTVSHIE 669
 Db 482 CGAQMVLGGRKEFKLNMKVTRLTDYALQPAVLODE-----TOSITQRLSFSPNQ 532

QY 670 GYECPQIFLVNLEAIEPGVYCAGHDNNNOPSFAAIISSNLELGERQVHVVKWAKALPGF 729
 Db 533 EIPFVPMPISVTRGIEPEVYAGVONTKPTPSSUITSHLICRQLCVVKSKLLE 592

QY 730 RNLHVDQMQAVIQYSWMGLVFMAGWRSFTINVSMLYFAPDLYNEYRMHSRMSYSCV 789
 Db 593 RNLHIDQTILIQYSWMSLNAFANGMRSYKHSQMLYFAPDILNEORMKESFYSCLL 652

QY 790 RMRHLSQEFGWLIQTPQEFLCMKALLFESTIPVGDLKKNKFEDELMRNKYKEDRILACK 849
 Db 653 SMWQDQEFTVRLQVSQEEFCMKAELLNIPLEGRLRSQFDMDRTSYIRELYKAIGLR 712

QY 850 RKNPTSCSRFRYQLTKLDSVQPIARELHQFTDLIKSHMSVDFPMMMAETISVQVPK 909

Science 237, 268-275, 1987
 A;Title: Cloning of human mineralocorticoid receptor complementary DNA: structural
 A;Accession number: A29513; MUID:87263386
 A;Molecule type: mRNA
 A;Residues: 1-84 <ARR>
 A;Cross-references: GB:M16801; NID:9187460; PTDN:AAA59571.1; PID:9307166
 C;Genetics:
 A;Gene: GDB:MLR
 A;Cross-references: GDB:120188; OMIM:264350
 A;Map position: 4q31-4q31
 C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
 C;Keywords: DNA binding; transcription regulation; zinc finger
 F;601-880:domain: erbA; transforming protein homology <ERBA>
 F;630-663:Region: zinc finger
 F;639-663:Region: zinc finger

Query Match 22.0%; Score 1078.5; DB 2; Length 984;
 Best Local Similarity 32.8%; Pred. No. 1..1e-49;
 Matches 300; Conservative 101; Mismatches 254; Gaps 30;

QY 98 SPQAHRGRTGYL-----VLDIEQQP-SOPOSALLECHPERGVPEP-----GAAYAAASK 145
 Db 238 SPNAENRGSRSHSPAHASNVGSPFLSSPLSSMMKSTISSPPSHOSVKSEPVSSPNNTVLRSSV 297

QY 146 GLPQQL-----PAPPDEDD-----SAAPSTL-SLLGP-----TFPGLSSCSADLKD 185
 Db 298 SSPANINNSRCSVSSPSATNNRSTLSSPAASITGSCSICSPVNNAFYSTASGTSAG357

QY 186 ILSEASTNOLLQQQ-----QQEAVSEGSSSGRA-----REASGAPTSKDNLYLGTT 231
 Db 358 WVPSPDTEQKGAEVQPFKTEVESEAISNGYTQQLNIVQYTKPEPDGFASSS--CLGGN 414

QY 232 STISDNAKELKAVASVSNGLGVYALEHLSPEQFLRGDCMYAPLGLYPVPAVRPTCAPLAE 291
 Db 415 SKINSDS-----SFSVPTIKOSTKUSCGTSFRGN-----PVNPFP-----451

QY 292 CKGSLDDDSAGKSAGTSDFAEY-----SPFGFCGTYKGLGEGLSGCSAAAGSSGTLLEPLSTL 349
 Db 452 --EMGCSYFSMDKDYYSLSGILGPPVPGFDG--NEBG5-----487

QY 350 YKGALDEAAQYSRDYYNFPLALAGPPPPPFPHPHARIKLENPLDYGSAAAAAACR 409
 Db 488 -----GFPVGIRQEP-----DDGS-----501

QY 410 YGDLASLHGAGAAAGPSGSGPAAASSSWHILFTAEGQLYGPCCGGGGGGGGGGGGGG 469
 Db 502 YYPEASIPSSAIVGVNSG-----GOFSHY-----525

QY 526 -----RIGAQTSLSRSRQDSRQH-----ESFP-EVNTLVE-----559

QY 530 WMDSYSGCPYGDMLRLETARDHVLPTDYYFP-----PQKTCLIGDGEASG 572

Db 560 WKS-----HGD-----LSSRRSDGYPLEIPEVNVSSTLRSVTSRSPSKTCLVGDEASG 612

QY 573 CHYGALTGCSCKVFKKRAARGKQKYLCASENDCTIDKFRRKNCSCURKCYBAGMTLGA 632

Db 613 CHYGVVTGCSCKVFKKRAVEQOHNLCAGRNDCLIDKLRKNCFACRLQCLQAGMNGLGA 672

QY 633 RKLKLNKL_LQERGEAASS-----TISPTBETT-----QLTVSH 667

Db 673 RKSKKKGKLGKIHEDPOQQQPPPPQQPSPECETTYTAPAKEPSNTALVFLQPSLTSR 732

QY 668 IEGYECQPIFLNVEIAIEPGVYCAGHDNNNQDPSFAALLSSNLEGERQLVHVVKWAKALP 727

Db 733 ---ALTPSPMVILENIEPIVYVYGDSSSKPDTAENLJSLTRLAGQMIOVVKWAKVLP 788

QY 728 GFNRLHVDQMAVILQYSWNLGMFAMGWSFTNNNSRMLYFADLVNEYRAHKSRMYSQCYRMHLS 787

Db 789 GFKNLPLEDQITLQYQSMCILSSALSALWSYKITSQLYFADLVNEEKHQSAMYELCQGMQIS 789

ULT 14
 513
 mineralocorticoid receptor - human
 1;Intername: aldosterone receptor
 1;Species: Homo sapiens (man)
 1;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
 1;Revision: A29513
 1;Owner: Weinberger, J.L.; Cerelli, G.; Glaser, T.M.; Housman, D.E.

QY	788	CYRMHLSQEFGWQIITPOEFUCMKALLFLSIIPYDGLKNOKEFDELMNYIKELDRTA	847
Db	849	CGGMHQISLQFVRQLTIEEYTIMKLLLSTIPKGQLSKQAEEFRNVTKLRAVAT	908
QY	848	CKRKNPCTCSRFEYQTYQDLSVQPTAREHQETFLIKSHMVSDFPMMAEITSVQ	907
Db	909	KCPNGNSGWSQREYQTKLDSMHDLVSLLEFCFTYTFRESHALKVEFPAMLVEILSDQL	968
QY	908	PKLSGKYKPIYFH	921
Db	969	PKVESGNAKPLYTH	982
RESULT 15			
QRPICG glucocorticoid receptor - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 31-Mar-1988 #sequence-revision 31-Mar-1988 #text-change 22-Jun-1999			
C:Accession: A24194 ; S02475 ; A27284 ; S33891 ; S33888 ; S02475 ; P02475 ; R:Miscellaneous, R:; Rusconi, S.; Godowski, P.J.; Maler, B.A.; Okret, S.; Wikstrom, A.C.; Gell, I.; Wieland, S.; Schaffner, W.; Rusconi, S.			
Cell:46, 389-399, 1986			
A:Title: Genetic complementation of a glucocorticoid receptor deficiency by expression			
A:Reference number: A24194 ; MUID:86272086			
A:Accession: A24194			
A:Molecule type: mRNA			
A:Residues: 1-795 <M1E>			
A:Cross-references: GB: M14053 ; NID:9204271 ; PIDN:AAA41203.1 ; PID:9204272			
R:Severne, Y.; Wieland, S.; Rusconi, S.			
EMBO J. 7, 250-2508, 1988			
A:Title: Metal binding 'finger' structures in the glucocorticoid receptor defined by s			
A:Reference number: S02475 ; MUID:89052664			
A:Accession: S02475			
A:Status: not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 440-539 <SEV>			
R:Chang, C.; Kokontis, J.; Chang, C.T.; Liao, S.			
Nucleic Acids Res. 15, 9603, 1987			
A:Title: Cloning and sequence analysis of the rat ventral prostate glucocorticoid rece			
A:Reference number: A27284 ; MUID:88067783			
A:Accession: A27284			
A:Molecule type: mRNA			
A:Residues: 1-97 ; D, '99-225,'G,'227-259,'D,'261-344,'T,'346-515 <CHA>			
A:Cross-references: GB:Y00489 ; NID:956234 ; PIDN:CAA68545.1 ; PID:g56325			
R:Gearing, K.L.; Gustafson, J.A.; Okret, S.			
Nucleic Acids Res. 21, 2014, 1993			
A:Title: Heterogeneity in the polyglutamine tract of the glucocorticoid receptor from			
A:Reference number: S33898 ; MUID:93261843			
A:Accession: S33888			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 68-92, '97,'D,'99-104 <GEA>			
A:Cross-references: EMBL:X69666			
A:Accession: S33891			
A:Status: preliminary			
C:Superfamily: glucocorticoid receptor; erbA transforming protein homology <ERBA>			
C:Molecule type: DNA			
A:Residues: 68-92, '97,'D,'99-104 <GEA>			
A:Cross-references: EMBL:X69669			
C:Comment: This sequence contains five potential translation initiators: 1-Met, 28-Met, d is initiated from 1-Met.			
F:7-96:Region: glutamine-rich			
F:438-692:Domain: erbA transforming protein homology <ERBA>			
F:440-460:Region: zinc finger CCCC motif			
F:446-500:Region: zinc finger CCCC motif			

Search completed: January 3, 2002, 23:07:40
Job time: 836 sec

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Best Local Similarity	21.78%	Pred. No. 4.5e-296.		
Best Local Similarity	32.08%	Mismatches 268.		
Best Local Similarity	32.08%	Indels 288.		
Best Local Similarity	32.08%	Gaps 35.		